

SEQUENCE LISTING

TO640x
(1) GENERAL INFORMATION:

(i) APPLICANT: RADIN, DAVID N.
CRAMER, CAROLE L.
OISHI, KAREN K.
WEISSENBOERN, DEBORAH L.

(ii) TITLE OF INVENTION: PRODUCTION OF LYSOSOMAL ENZYMES IN
PLANT-BASED EXPRESSION SYSTEMS

(iii) NUMBER OF SEQUENCES: 15

(iv) CORRESPONDENCE ADDRESS:

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(E) COUNTRY: USA
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(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

B
(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/713,928
(B) FILING DATE: 13-SEP-1996
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/003,737
(B) FILING DATE: 14-SEP-1995

(viii) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 30,742
(C) REFERENCE/DOCKET NUMBER: 7956-0011-999

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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTGTCTAGAG TAAGCATCAT GGCTGGC

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CACGAATTCT GGCGACGCCA CAGGTAGGTG TGA

33

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1642 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGAGTTTT CAAGTCCTTC CAGAGAGGAA TGTCCCAAGC CTTTGAGTAG GGTAAGCATC	60
ATGGCTGGCA GCCTCACAGG TTTGCTTCTA CTTCAGGCAG TGTCGTGGGC ATCAGGTGCC	120
CGCCCCTGCA TCCCTAAAAG CTTCGGCTAC AGCTCGGTGG TGTGTGTCTG CAATGCCACA	180
TACTGTGACT CCTTTGACCC CCCGACCTTT CCTGCCCTTG GTACCTTCAG CCGCTATGAG	240
AGTACACGCA GTGGGCGACG GATGGGGCTG AGTATGGGGC CCATCCAGGC TAATCACACG	300
GGCACAGGCC TGCTACTGAC CCTGCAGCCA GAACAGAAGT TCCAGAAAGT GAAGGGATTT	360
GGAGGGGCCA TGACAGATGC TGCTGCTCTC AACATCCTTG CCCTGTCACC CCCTGCCCAA	420
AATTTGCTAC TTAAATCGTA CTTCTCTGAA GAAGGAATCG GATATAACAT CATCCGGGTA	480
CCCATGGCCA GCTGTGACTT CTCCATCCGC ACCTACACCT ATGCAGACAC CCCTGATGAT	540
TTCCAGTTGC ACAACTTCAG CCTCCCAGAG GAAGATACCA AGCTCAAGAT ACCCCTGATT	600
CACCGAGCCC TGCAGTTGGC CCAGCGTCCC GTTTCACTCC TTGCCAGCCC CTGGACATCA	660
CCCCTTGGC TCAAGACCAA TGGAGCGGTG AATGGGAAGG GGTCCTCAA GGGACAGCCC	720
GGAGACATCT ACCACCAGAC CTGGGCCAGA TACTTTGTGA AGTTCCTGGA TGCCTATGCT	780
GAGCACAAGT TACAGTTCTG GGCAGTGACA GCTGAAAATG AGCCTTCTGC TGGGCTGTTG	840
AGTGATAACC CCTTCCAGTG CCTGGGCTTC ACCCCTGAAC ATCAGCGAGA CTTCATTGCC	900
CGTGACCTAG GTCCTACCTT CGCCAACAGT ACTCACCACA ATGTCCGCCT ACTCATGCTG	960
GATGACCAAC GCTTGCTGCT GCCCACTGG GCAAAGGTGG TACTGACAGA CCCAGAAGCA	1020

GCTAAATATG TTCATGGCAT TGCTGTACAT TGGTACCTGG ACTTTCTGGC TCCAGCCAAA 1080
 GCCACCCTAG GGGAGACACA CCGCCTGTTT CCCAACACCA TGCTCTTTGC CTCAGAGGCC 1140
 TGTGTGGGCT CCAAGTTCTG GGAGCAGAGT GTGCGGCTAG GCTCCTGGGA TCGAGGGATG 1200
 CAGTACAGCC ACAGCATCAT CACGAACCTC CTGTACCATG TGGTCGGCTG GACCGACTGG 1260
 AACCTTGCCC TGAACCCCGA AGGAGGACCC AATTGGGTGC GTAACCTTGT CGACAGTCCC 1320
 ATCATTGTAG ACGTCACCAG GGACACGTTT TACAAACAGC CCATGTTCTA CCACCTTGGC 1380
 CACTTCAGCA AGTTCATTCC TGAGGGCTCC CAGAGAGTGG GGCTGGTTGC CAGTCAGAAG 1440
 AACGACCTGG ACGCAGTGGC ACTGATGCAT CCCGATGGCT CTGCTGTTGT GGTCGTGCTA 1500
 AACCGCTCCT CTAAGGATGT GCCTCTTACC ATCAAGGATC CTGCTGTGGG CTTCCTGGAG 1560
 ACAATCTCAC CTGGCTACTC CATTACACC TACCTGTGGC GTCGCCAGAA TTCGGACTAC 1620
 AAGGACGACG ATGACAAGTT GA 1642

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 546 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Glu	Phe	Ser	Ser	Pro	Ser	Arg	Glu	Glu	Cys	Pro	Lys	Pro	Leu	Ser	1	5	10	15
Arg	Val	Ser	Ile	Met	Ala	Gly	Ser	Leu	Thr	Gly	Leu	Leu	Leu	Leu	Gln	20	25	30	
Ala	Val	Ser	Trp	Ala	Ser	Gly	Ala	Arg	Pro	Cys	Ile	Pro	Lys	Ser	Phe	35	40	45	
Gly	Tyr	Ser	Ser	Val	Val	Cys	Val	Cys	Asn	Ala	Thr	Tyr	Cys	Asp	Ser	50	55	60	
Phe	Asp	Pro	Pro	Thr	Phe	Pro	Ala	Leu	Gly	Thr	Phe	Ser	Arg	Tyr	Glu	65	70	75	80
Ser	Thr	Arg	Ser	Gly	Arg	Arg	Met	Glu	Leu	Ser	Met	Gly	Pro	Ile	Gln	85	90	95	
Ala	Asn	His	Thr	Gly	Thr	Gly	Leu	Leu	Leu	Thr	Leu	Gln	Pro	Glu	Gln	100	105	110	
Lys	Phe	Gln	Lys	Val	Lys	Gly	Phe	Gly	Gly	Ala	Met	Thr	Asp	Ala	Ala	115	120	125	
Ala	Leu	Asn	Ile	Leu	Ala	Leu	Ser	Pro	Pro	Ala	Gln	Asn	Leu	Leu	Leu	130	135	140	
Lys	Ser	Tyr	Phe	Ser	Glu	Gly	Ile	Gly	Tyr	Asn	Ile	Ile	Arg	Val		145	150	155	160

Pro Met Ala Ser Cys Asp Phe Ser Ile Arg Thr Tyr Thr Tyr Ala Asp
 165 170 175
 Thr Pro Asp Asp Phe Gln Leu His Asn Phe Ser Leu Pro Glu Glu Asp
 180 185 190
 Thr Lys Leu Lys Ile Pro Leu Ile His Arg Ala Leu Gln Leu Ala Gln
 195 200 205
 Arg Pro Val Ser Leu Leu Ala Ser Pro Trp Thr Ser Pro Thr Trp Leu
 210 215 220
 Lys Thr Asn Gly Ala Val Asn Gly Lys Gly Ser Leu Lys Gly Gln Pro
 225 230 235 240
 Gly Asp Ile Tyr His Gln Thr Trp Ala Arg Tyr Phe Val Lys Phe Leu
 245 250 255
 Asp Ala Tyr Ala Glu His Lys Leu Gln Phe Trp Ala Val Thr Ala Glu
 260 265 270
 Asn Glu Pro Ser Ala Gly Leu Leu Ser Gly Tyr Pro Phe Gln Cys Leu
 275 280 285
 Gly Phe Thr Pro Glu His Gln Arg Asp Phe Ile Ala Arg Asp Leu Gly
 290 295 300
 Pro Thr Leu Ala Asn Ser Thr His His Asn Val Arg Leu Leu Met Leu
 305 310 315 320
 Asp Asp Gln Arg Leu Leu Leu Pro His Trp Ala Lys Val Val Leu Thr
 325 330 335
 Asp Pro Glu Ala Ala Lys Tyr Val His Gly Ile Ala Val His Trp Tyr
 340 345 350
 Leu Asp Phe Leu Ala Pro Ala Lys Ala Thr Leu Gly Glu Thr His Arg
 355 360 365
 Leu Phe Pro Asn Thr Met Leu Phe Ala Ser Glu Ala Cys Val Gly Ser
 370 375 380
 Lys Phe Trp Glu Gln Ser Val Arg Leu Gly Ser Trp Asp Arg Gly Met
 385 390 395 400
 Gln Tyr Ser His Ser Ile Ile Thr Asn Leu Leu Tyr His Val Val Gly
 405 410 415
 Trp Thr Asp Trp Asn Leu Ala Leu Asn Pro Glu Gly Gly Pro Asn Trp
 420 425 430
 Val Arg Asn Phe Val Asp Ser Pro Ile Ile Val Asp Val Thr Lys Asp
 435 440 445
 Thr Phe Tyr Lys Gln Pro Met Phe Tyr His Leu Gly His Phe Ser Lys
 450 455 460
 Phe Ile Pro Glu Gly Ser Gln Arg Val Gly Leu Val Ala Ser Gln Lys
 465 470 475 480
 Asn Asp Leu Asp Ala Val Ala Leu Met His Pro Asp Gly Ser Ala Val
 485 490 495
 Val Val Val Leu Asn Arg Ser Ser Lys Asp Val Pro Leu Thr Ile Lys
 500 505 510
 Asp Pro Ala Val Gly Phe Leu Glu Thr Ile Ser Pro Gly Tyr Ser Ile

515

520

525

His Thr Tyr Leu Trp Arg Arg Gln Asn Ser Asp Tyr Lys Asp Asp Asp
 530 535 540

Asp Lys
 545

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "MeGA Promoter"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CAATACGATA TTACCGAATA TTATACTAAA TCAAAATTTA ATTTATCATA TCGAATTATT	60
AAACTGATAT TTCAAATTTT AATATTTAAT ATCTACTTTC AACTATTATT ACCTAATTAT	120
CAAATGCAAA ATGTATGAGT TATTTTCATA TAGCCCGAGT TCGTATCCAA ATATTTTACA	180
CTTGACCACT CAACTTGACT ATATAAACT TTAATTTCAA AAATTAATAA AAAAAGAAAG	240
TATATTATTG TAAAAGATAA TACTCCATTC AAAATATAAA ATGAAAAAAG TCCAGCGCGG	300
CAACCGGGTT CCTCTATAAA TACATTTCTT ACATCTTCTC TTCTCCTCAC ATCCCATCAC	360
TCTTCTTTTA ACAATTATAC TTGTCAATCA TCAATCCCAC AAACAACACT TTTTCTCTCC	420
TCTTTTTCCT CACCGGCGGC AGACTTACCG GTGAAATCTA GAGTAAGCAT C	471

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 32 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

- (A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CTAGTCTAGA ATGCGTCCCC TCGCCCCCG CG	32
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(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

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(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GGAATTCGAG CTCTCATGGA TTGCCCCGGG ATG

33

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 2067 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: unknown
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGCGTCCCC	TGCGCCCCCG	CGCCGCGCTG	CTGGCGCTCC	TGGCCTCGCT	CCTGGCCGCG	60
CCCCCGGTGG	CCCCGGCCGA	GGCCCCGCAC	CTGGTGCAGG	TGGACGCGGC	CCGCGCGCTG	120
TGGCCCCCTGC	GGCGCTTCTG	GAGGAGCACA	GGCTTCTGCC	CCCCGCTGCC	ACACAGCCAG	180
GCTGACCAGT	ACGTCCTCAG	CTGGGACCAG	CAGCTCAACC	TCGCCTATGT	GGGCGCCGTC	240
CCTCACC GCG	GCATCAAGCA	GGTCCGGACC	CACTGGCTGC	TGGAGCTTGT	CACCACCAGG	300
GGGTCCACTG	GACGGGGCCT	GAGCTACAAC	TTCACCCACC	TGGACGGGTA	CTTGGACCTT	360
CTCAGGGAGA	ACCAGCTCCT	CCCAGGGTTT	GAGCTGATGG	GCAGCGCCTC	GGGCCACTTC	420
ACTGACTTTG	AGGACAAGCA	GCAGGTGTTT	GAGTGAAGG	ACTTGGTCTC	CAGCCTGGCC	480
AGGAGATACA	TCGGTAGGTA	CGGACTGGCG	CATGTTTCCA	AGTGGAAGTT	CGAGACGTGG	540
AATGAGCCAG	ACCACCACGA	CTTTGACAAC	GTCTCCATGA	CCATGCAAGG	CTTCCTGAAC	600
TACTACGATG	CCTGCTCGGA	GGGTCTGCGC	GCCGCCAGCC	CCGCCCTGCG	GCTGGGAGGC	660
CCCCGGCGACT	CCTTCCACAC	CCCACCGCGA	TCCCCGCTGA	GCTGGGGCCT	CCTGCGCCAC	720
TGCCACGACG	GTACCAACTT	CTTCACTGGG	GAGGCGGGCG	TGCGGCTGGA	CTACATCTCC	780
CTCCACAGGA	AGGGTGCGCG	CAGCTCCATC	TCCATCCTGG	AGCAGGAGAA	GGTCGTGCGG	840
CACGAGATCC	GGCAGCTCTT	CCCCAAGTTC	GCGGACACCC	CCATTTACAA	CGACGAGGCG	900
GACCCGCTGG	TGGGCTGGTC	CCTGCCACAG	CCGTGGAGGG	CGGACGTGAC	CTACGCGGCC	960
ATGGTGGTGA	AGGTCATCGC	GCAGCATCAG	AACCTGCTAC	TGGCCAACAC	CACCTCCGCC	1020
TTCCCCTACG	CGCTCCTGAG	CAACGACAAT	GCCTTCCTGA	GCTACCACCC	GCACCCCTTC	1080
GCGCAGCGCA	CGCTCACC GC	GCGCTTCCAG	GTCAACAACA	CCCCCCCGCC	GCACGTGCAG	1140
CTGTTGCGCA	AGCCGGTGCT	CACGGCCATG	GGGCTGCTGG	CGCTGCTGGA	TGAGGAGCAG	1200
CTCTGGGCCG	AAGTGTCGCA	GGCCGGGACC	GTCCTGGACA	GCAACCACAC	GGTGGGCGTC	1260

CTGGCCAGCG CCCACCGCCC CCAGGGCCCC GCCGACGCCT GCGCGCGCCG GGTGCTGATC	1320
TACGCGAGCG ACGACACCCG CGCCACCCC AACCGCAGCG TCGCGGTGAC CCTGCGGCTG	1380
CGCGGGGTGC CCCCCGCCCC GGGCCTGGTC TACGTCACGC GCTACCTGGA CAACGGGCTC	1440
TGCAGCCCCG ACGGCGAGTG GCGGCGCCTG GGCCGGCCCC TCTTCCCCAC GGCAGAGCAG	1500
TTCCGGCGCA TGCGCGCGGC TGAGGACCCG GTGGCCGCGG CGCCCCGCCC CTTACCCGCC	1560
GGCGGCCGCC TGACCCTGCG CCCC CGCGCTG CGGCTGCCGT CGCTTTTGCT GGTGCACGTG	1620
TGTGCGCGCC CCGAGAAGCC GCCCCGGGCG GTCACGCGGC TCCGCGCCCT GCCCCTGACC	1680
CAAGGGCAGC TGGTTCTGGT CTGGTCGGAT GAACACGTGG GCTCCAAGTG CCTGTGGACA	1740
TACGAGATCC AGTTCTCTCA GGACGGTAAG GCGTACACCC CGGTCAGCAG GAAGCCATCG	1800
ACCTTCAACC TCTTTGTGTT CAGCCCAGAC ACAGGTGCTG TCTCTGGCTC CTACCGAGTT	1860
CGAGCCCTGG ACTACTGGGC CCGACCAGGC CCCTTCTCGG ACCCTGTGCC GTACCTGGAG	1920
GTCCCTGTGC CAAGAGGGCC CCCATCCCCG GGCAATCCAT GAGCCTGTGC TGAGCCCCAG	1980
TGGGTTGCAC CTCCACCGGC AGTCAGCGAG CTGGGGCTGC ACTGTGCCCCA TGCTGCCCTC	2040
CCATCACCCC CTTTGCAATA TATTTT	2067

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 653 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Arg	Pro	Leu	Arg	Pro	Arg	Ala	Ala	Leu	Leu	Ala	Leu	Leu	Ala	Ser	1	5	10	15
Leu	Leu	Ala	Ala	Pro	Pro	Val	Ala	Pro	Ala	Glu	Ala	Pro	His	Leu	Val	20	25	30	
His	Val	Asp	Ala	Ala	Arg	Ala	Leu	Trp	Pro	Leu	Arg	Arg	Phe	Trp	Arg	35	40	45	
Ser	Thr	Gly	Phe	Cys	Pro	Pro	Leu	Pro	His	Ser	Gln	Ala	Asp	Gln	Tyr	50	55	60	
Val	Leu	Ser	Trp	Asp	Gln	Gln	Leu	Asn	Leu	Ala	Tyr	Val	Gly	Ala	Val	65	70	75	80
Pro	His	Arg	Gly	Ile	Lys	Gln	Val	Arg	Thr	His	Trp	Leu	Leu	Glu	Leu	85	90	95	
Val	Thr	Thr	Arg	Gly	Ser	Thr	Gly	Arg	Gly	Leu	Ser	Tyr	Asn	Phe	Thr	100	105	110	
His	Leu	Asp	Gly	Thr	Leu	Asp	Leu	Leu	Arg	Glu	Asn	Gln	Leu	Leu	Pro	115	120	125	

Gly	Phe	Glu	Leu	Met	Gly	Ser	Ala	Ser	Gly	His	Phe	Thr	Asp	Phe	Glu
130						135					140				
Asp	Lys	Gln	Gln	Val	Phe	Glu	Trp	Lys	Asp	Leu	Val	Ser	Ser	Leu	Ala
145					150					155					160
Arg	Arg	Tyr	Ile	Gly	Arg	Tyr	Gly	Leu	Ala	His	Val	Ser	Lys	Trp	Asn
				165					170					175	
Phe	Glu	Thr	Trp	Asn	Glu	Pro	Asp	His	His	Asp	Phe	Asp	Asn	Val	Ser
			180					185					190		
Met	Thr	Met	Gln	Gly	Phe	Leu	Asn	Tyr	Tyr	Asp	Ala	Cys	Ser	Glu	Gly
		195					200					205			
Leu	Arg	Ala	Ala	Ser	Pro	Ala	Leu	Arg	Leu	Gly	Gly	Pro	Gly	Asp	Ser
	210					215					220				
Phe	His	Thr	Pro	Pro	Arg	Ser	Pro	Leu	Ser	Trp	Gly	Leu	Leu	Arg	His
225					230					235					240
Cys	His	Asp	Gly	Thr	Asn	Phe	Phe	Thr	Gly	Glu	Ala	Gly	Val	Arg	Leu
				245					250					255	
Asp	Tyr	Ile	Ser	Leu	His	Arg	Lys	Gly	Ala	Arg	Ser	Ser	Ile	Ser	Ile
			260					265					270		
Leu	Glu	Gln	Glu	Lys	Val	Val	Ala	Gln	Glu	Ile	Arg	Gln	Leu	Phe	Pro
	275						280					285			
Lys	Phe	Ala	Asp	Thr	Pro	Ile	Tyr	Asn	Asp	Glu	Ala	Asp	Pro	Leu	Val
	290					295					300				
Gly	Trp	Ser	Leu	Pro	Gln	Pro	Trp	Arg	Ala	Asp	Val	Thr	Tyr	Ala	Ala
305					310					315					320
Met	Val	Val	Lys	Val	Ile	Ala	Gln	His	Gln	Asn	Leu	Leu	Leu	Ala	Asn
				325					330					335	
Thr	Thr	Ser	Ala	Phe	Pro	Tyr	Ala	Leu	Leu	Ser	Asn	Asp	Asn	Ala	Phe
			340					345					350		
Leu	Ser	Tyr	His	Pro	His	Pro	Phe	Ala	Gln	Arg	Thr	Leu	Thr	Ala	Arg
		355					360					365			
Phe	Gln	Val	Asn	Asn	Thr	Arg	Pro	Pro	His	Val	Gln	Leu	Leu	Arg	Lys
	370					375					380				
Pro	Val	Leu	Thr	Ala	Met	Gly	Leu	Leu	Ala	Leu	Leu	Asp	Glu	Glu	Gln
385					390					395					400
Leu	Trp	Ala	Glu	Val	Ser	Gln	Ala	Gly	Thr	Val	Leu	Asp	Ser	Asn	His
				405					410					415	
Thr	Val	Gly	Val	Leu	Ala	Ser	Ala	His	Arg	Pro	Gln	Gly	Pro	Ala	Asp
			420					425					430		
Ala	Trp	Arg	Ala	Ala	Val	Leu	Ile	Tyr	Ala	Ser	Asp	Asp	Thr	Arg	Ala
		435					440					445			
His	Pro	Asn	Arg	Ser	Val	Ala	Val	Thr	Leu	Arg	Leu	Arg	Gly	Val	Pro
	450					455					460				
Pro	Gly	Pro	Gly	Leu	Val	Tyr	Val	Thr	Arg	Tyr	Leu	Asp	Asn	Gly	Leu
465					470					475					480
Cys	Ser	Pro	Asp	Gly	Glu	Trp	Arg	Arg	Leu	Gly	Arg	Pro	Val	Phe	Pro

485								490				495			
Thr	Ala	Glu	Gln	Phe	Arg	Arg	Met	Arg	Ala	Ala	Glu	Asp	Pro	Val	Ala
			500						505				510		
Ala	Ala	Pro	Arg	Pro	Leu	Pro	Ala	Gly	Gly	Arg	Leu	Thr	Leu	Arg	Pro
		515					520					525			
Ala	Leu	Arg	Leu	Pro	Ser	Leu	Leu	Val	His	Val	Cys	Ala	Arg	Pro	
	530					535				540					
Glu	Lys	Pro	Pro	Gly	Gln	Val	Thr	Arg	Leu	Arg	Ala	Leu	Pro	Leu	Thr
545					550					555					560
Gln	Gly	Gln	Leu	Val	Leu	Val	Trp	Ser	Asp	Glu	His	Val	Gly	Ser	Lys
			565						570					575	
Cys	Leu	Trp	Thr	Tyr	Glu	Ile	Gln	Phe	Ser	Gln	Asp	Gly	Lys	Ala	Tyr
			580					585					590		
Thr	Pro	Val	Ser	Arg	Lys	Pro	Ser	Thr	Phe	Asn	Leu	Phe	Val	Phe	Ser
		595					600					605			
Pro	Asp	Thr	Gly	Ala	Val	Ser	Gly	Ser	Tyr	Arg	Val	Arg	Ala	Leu	Asp
	610					615					620				
Tyr	Trp	Ala	Arg	Pro	Gly	Pro	Phe	Ser	Asp	Pro	Val	Pro	Tyr	Leu	Glu
625					630					635					640
Val	Pro	Val	Pro	Arg	Gly	Pro	Pro	Ser	Pro	Gly	Asn	Pro			
				645					650						

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 8 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid
(A) DESCRIPTION: /desc = "PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GCCTATGCTG AGCACAAGTT ACAG

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "Complementary sequence of a PCR primer"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCCCTTGAGC TCGTCACTGG CGACGCCACA GGTA

34

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 48 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CAGAATTCGG ACTACAAGGA CGACGATGAC AAGTAGGAGC TCGAATTC

48

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Asn Ser Asp Tyr Lys Asp Asp Asp Asp Lys
1 5 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 4 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Lys Asp Glu Leu
1